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## RAW SEQUENCE LISTING

DATE: 04/12/2002

PATENT APPLICATION: US/09/898,751A

TIME: 15:01:06

Input Set : A:\DX0882XKseq1stg.txt

Output Set: N:\CRF3\04122002\I898751A.raw

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3 <110> APPLICANT: Oldham, Elizabeth R.
4      Soto, Hortensia
5      Liu, Ying
6      Hudak, Susan A.
7      Homey, Bernhard
8      Morales, Janine M.
9      Kellerman, Sirid-Aimee
10     McEvoy, Leslie M.
11     Bowman, Edward P.
12     Zlotnik, Albert
14 <120> TITLE OF INVENTION: CHEMOKINE AND RECEPTOR USES; COMPOSITIONS; METHODS
16 <130> FILE REFERENCE: DX0882XK
C--> 18 <140> CURRENT APPLICATION NUMBER: US/09/898,751A
19 <141> CURRENT FILING DATE: 2001-07-02
21 <150> PRIOR APPLICATION NUMBER: US09/471,549
22 <151> PRIOR FILING DATE: 1999-12-23
24 <150> PRIOR APPLICATION NUMBER: US60/136,570
25 <151> PRIOR FILING DATE: 1999-05-27
27 <150> PRIOR APPLICATION NUMBER: US60/113,858
28 <151> PRIOR FILING DATE: 1998-12-24
30 <160> NUMBER OF SEQ ID NOS: 16
32 <170> SOFTWARE: PatentIn version 3.1
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 1089
36 <212> TYPE: DNA
37 <213> ORGANISM: Homo sapiens
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40 <221> NAME/KEY: CDS
41 <222> LOCATION: (1)..(1086)
42 <223> OTHER INFORMATION:
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50 gat gaa gag gac gca tac tcg gct gag cca ctg ccg gag ctt tgc tac      96
51 Asp Glu Glu Asp Ala Tyr Ser Ala Glu Pro Leu Pro Glu Leu Cys Tyr
52          20          25          30
54 aag gcc gat gtc cag gcc ttc agc cgg gcc ttc caa ccc agt gtc tcc      144
55 Lys Ala Asp Val Gln Ala Phe Ser Arg Ala Phe Gln Pro Ser Val Ser
56          35          40          45
58 ctg acg ctg gct gcg ctg ggt ctg gcc ggc aat ggc ctg gtc ctg gcc      192
59 Leu Thr Leu Ala Ala Leu Gly Leu Ala Gly Asn Gly Leu Val Leu Ala
60          50          55          60

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62	acc	cac	ctg	gca	gcc	cga	cgc	gca	gcg	cgc	tcg	ccc	acc	tct	gcc	cac	240
63	Thr	His	Leu	Ala	Ala	Arg	Arg	Ala	Ala	Arg	Ser	Pro	Thr	Ser	Ala	His	
64	65					70					75					80	
66	ctg	ctc	cag	ctg	gcc	ctg	gcc	gac	ctc	ttg	ctg	gcc	ctg	act	ctg	ccc	288
67	Leu	Leu	Gln	Leu	Ala	Leu	Ala	Asp	Leu	Leu	Ala	Leu	Thr	Leu	Pro		
68					85					90					95		
70	ttc	gcg	gca	gca	ggg	gct	ctt	cag	ggc	tgg	agt	ctg	gga	agt	gcc	acc	336
71	Phe	Ala	Ala	Ala	Gly	Ala	Leu	Gln	Gly	Trp	Ser	Leu	Gly	Ser	Ala	Thr	
72				100					105					110			
74	tgc	cgc	acc	atc	tct	ggc	ctc	tac	tcg	gcc	tcc	ttc	cac	gcc	ggc	ttc	384
75	Cys	Arg	Thr	Ile	Ser	Gly	Leu	Tyr	Ser	Ala	Ser	Phe	His	Ala	Gly	Phe	
76			115					120						125			
78	ctc	ttc	ctg	gcc	tgt	atc	agc	gcc	gac	cgc	tac	gtg	gcc	atc	gcg	cga	432
79	Leu	Phe	Leu	Ala	Cys	Ile	Ser	Ala	Asp	Arg	Tyr	Val	Ala	Ile	Ala	Arg	
80		130						135					140				
82	gcg	ctc	cca	gcc	ggg	ccg	cgg	ccc	tcc	act	ccc	ggc	cgc	gca	cac	ttg	480
83	Ala	Leu	Pro	Ala	Gly	Pro	Arg	Pro	Ser	Thr	Pro	Gly	Arg	Ala	His	Leu	
84	145				150						155					160	
86	gtc	tcc	gtc	atc	gtg	tgg	ctg	ctg	tca	ctg	ctc	ctg	gcg	ctg	cct	gcg	528
87	Val	Ser	Val	Ile	Val	Trp	Leu	Leu	Ser	Leu	Leu	Leu	Ala	Leu	Pro	Ala	
88				165						170					175		
90	ctg	ctc	ttc	agc	cag	gat	ggg	cag	cgg	gaa	ggc	caa	cga	cgc	tgt	cgc	576
91	Leu	Leu	Phe	Ser	Gln	Asp	Gly	Gln	Arg	Glu	Gly	Gln	Arg	Arg	Cys	Arg	
92			180							185					190		
94	ctc	atc	ttc	ccc	gag	ggc	ctc	acg	cag	acg	gtg	aag	ggg	gcg	agc	gcc	624
95	Leu	Ile	Phe	Pro	Glu	Gly	Leu	Thr	Gln	Thr	Val	Lys	Gly	Ala	Ser	Ala	
96			195						200					205			
98	gtg	gcg	cag	gtg	gcc	ctg	ggc	ttc	gcg	ctg	ccg	ctg	ggc	gtc	atg	gta	672
99	Val	Ala	Gln	Val	Ala	Leu	Gly	Phe	Ala	Leu	Pro	Leu	Gly	Val	Met	Val	
100		210					215						220				
102	gcc	tgc	tac	gcg	ctt	ctg	ggc	cgc	acg	ctg	ctg	gcc	gcc	agg	ggg	ccc	720
103	Ala	Cys	Tyr	Ala	Leu	Leu	Gly	Arg	Thr	Leu	Leu	Ala	Ala	Arg	Gly	Pro	
104	225					230						235				240	
106	gag	cgc	cgg	cgt	gcg	ctg	cgc	gtc	gtg	gtg	gct	ctg	gtg	gcg	gcc	ttc	768
107	Glu	Arg	Arg	Arg	Ala	Leu	Arg	Val	Val	Val	Ala	Leu	Val	Ala	Ala	Phe	
108				245						250					255		
110	gtg	gtg	ctg	cag	ctg	ccc	tac	agc	ctc	gcc	ctg	ctg	ctg	gat	act	gcc	816
111	Val	Val	Leu	Gln	Leu	Pro	Tyr	Ser	Leu	Ala	Leu	Leu	Leu	Asp	Thr	Ala	
112				260						265					270		
114	gat	cta	ctg	gct	gcg	cgc	gag	cgg	agc	tgc	cct	gcc	agc	aaa	cgc	aag	864
115	Asp	Leu	Leu	Ala	Ala	Arg	Glu	Arg	Ser	Cys	Pro	Ala	Ser	Lys	Arg	Lys	
116			275						280					285			
118	gat	gtc	gca	ctg	ctg	gtg	acc	agc	ggc	ttg	gcc	ctc	gcc	cgc	tgt	ggc	912
119	Asp	Val	Ala	Leu	Leu	Val	Thr	Ser	Gly	Leu	Ala	Leu	Ala	Arg	Cys	Gly	
120		290				295						300					
122	ctc	aat	ccc	gtt	ctc	tac	gcc	ttc	ctg	ggc	ctg	cgc	ttc	cgc	cag	gac	960
123	Leu	Asn	Pro	Val	Leu	Tyr	Ala	Phe	Leu	Gly	Leu	Arg	Phe	Arg	Gln	Asp	
124	305					310					315				320		
126	ctg	cgg	agg	ctg	cta	cgg	ggt	ggg	agc	tcg	ccc	tca	ggg	cct	caa	ccc	1008

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128          325          330          335
130 cgc cgc ggc tgc ccc cgc cgg ccc cgc ctt tct tcc tgc tca gct ccc 1056
131 Arg Arg Gly Cys Pro Arg Arg Pro Arg Leu Ser Ser Cys Ser Ala Pro
132          340          345          350
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135 Thr Glu Thr His Ser Leu Ser Trp Asp Asn
136          355          360
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147 1          5          10          15
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151          20          25          30
154 Lys Ala Asp Val Gln Ala Phe Ser Arg Ala Phe Gln Pro Ser Val Ser
155          35          40          45
158 Leu Thr Leu Ala Ala Leu Gly Leu Ala Gly Asn Gly Leu Val Leu Ala
159          50          55          60
162 Thr His Leu Ala Ala Arg Arg Ala Ala Arg Ser Pro Thr Ser Ala His
163 65          70          75          80
166 Leu Leu Gln Leu Ala Leu Ala Asp Leu Leu Leu Ala Leu Thr Leu Pro
167          85          90          95
170 Phe Ala Ala Ala Gly Ala Leu Gln Gly Trp Ser Leu Gly Ser Ala Thr
171          100          105          110
174 Cys Arg Thr Ile Ser Gly Leu Tyr Ser Ala Ser Phe His Ala Gly Phe
175          115          120          125
178 Leu Phe Leu Ala Cys Ile Ser Ala Asp Arg Tyr Val Ala Ile Ala Arg
179          130          135          140
182 Ala Leu Pro Ala Gly Pro Arg Pro Ser Thr Pro Gly Arg Ala His Leu
183 145          150          155          160
186 Val Ser Val Ile Val Trp Leu Leu Ser Leu Leu Leu Ala Leu Pro Ala
187          165          170          175
190 Leu Leu Phe Ser Gln Asp Gly Gln Arg Glu Gly Gln Arg Arg Cys Arg
191          180          185          190
194 Leu Ile Phe Pro Glu Gly Leu Thr Gln Thr Val Lys Gly Ala Ser Ala
195          195          200          205
198 Val Ala Gln Val Ala Leu Gly Phe Ala Leu Pro Leu Gly Val Met Val
199          210          215          220
202 Ala Cys Tyr Ala Leu Leu Gly Arg Thr Leu Leu Ala Ala Arg Gly Pro
203 225          230          235          240
206 Glu Arg Arg Arg Ala Leu Arg Val Val Val Ala Leu Val Ala Ala Phe
207          245          250          255
210 Val Val Leu Gln Leu Pro Tyr Ser Leu Ala Leu Leu Leu Asp Thr Ala
211          260          265          270
214 Asp Leu Leu Ala Ala Arg Glu Arg Ser Cys Pro Ala Ser Lys Arg Lys
215          275          280          285

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218 Asp Val Ala Leu Leu Val Thr Ser Gly Leu Ala Leu Ala Arg Cys Gly
219      290      295      300
222 Leu Asn Pro Val Leu Tyr Ala Phe Leu Gly Leu Arg Phe Arg Gln Asp
223 305      310      315      320
226 Leu Arg Arg Leu Leu Arg Gly Gly Ser Ser Pro Ser Gly Pro Gln Pro
227      325      330      335
230 Arg Arg Gly Cys Pro Arg Arg Pro Arg Leu Ser Ser Cys Ser Ala Pro
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234 Thr Glu Thr His Ser Leu Ser Trp Asp Asn
235      355      360
238 <210> SEQ ID NO: 3
239 <211> LENGTH: 1089
240 <212> TYPE: DNA
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243 <220> FEATURE:
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246 <223> OTHER INFORMATION:
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252 1      5      10      15
254 tac gat gag gag gcc tat tcg gtt ggg ccg ctg cca gag ctc tgt tac      96
255 Tyr Asp Glu Glu Ala Tyr Ser Val Gly Pro Leu Pro Glu Leu Cys Tyr
256      20      25      30
258 aag gct gat gtc cag gct ttc agt cgg gcc ttc caa ccc agt gtc tcc      144
259 Lys Ala Asp Val Gln Ala Phe Ser Arg Ala Phe Gln Pro Ser Val Ser
260      35      40      45
262 ctg atg gtg gct gta ctg ggt ctg gct ggc aat ggc cta gtc ttg gcc      192
263 Leu Met Val Ala Val Leu Gly Leu Ala Gly Asn Gly Leu Val Leu Ala
264 50      55      60
266 acc cat ctg gca gcc aga cga act acc cga tct ccc acc tcc gtt cac      240
267 Thr His Leu Ala Ala Arg Arg Thr Thr Arg Ser Pro Thr Ser Val His
268 65      70      75      80
270 ctg ctc cag ttg gcc ctg gct gac ctt tta ttg gcc ctg act ttg cct      288
271 Leu Leu Gln Leu Ala Leu Ala Asp Leu Leu Leu Ala Leu Thr Leu Pro
272      85      90      95
274 ttt gct gca gca ggg gct ctt cag ggc tgg aat cta gga agt acc acc      336
275 Phe Ala Ala Ala Gly Ala Leu Gln Gly Trp Asn Leu Gly Ser Thr Thr
276      100      105      110
278 tgc cgt gcc atc tca ggc ctc tac tcg gcc tct ttc cac gct ggc ttc      384
279 Cys Arg Ala Ile Ser Gly Leu Tyr Ser Ala Ser Phe His Ala Gly Phe
280      115      120      125
282 ctc ttc cta gcc tgt atc agc gcc gac cgc tat gtg gcc atc gca cga      432
283 Leu Phe Leu Ala Cys Ile Ser Ala Asp Arg Tyr Val Ala Ile Ala Arg
284      130      135      140
286 gct ctc cca gcc ggg cag cgg ccc tca acg cct agc cga gcg cac ttg      480
287 Ala Leu Pro Ala Gly Gln Arg Pro Ser Thr Pro Ser Arg Ala His Leu
288 145      150      155      160

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Input Set : A:\DX0882XKseq1stg.txt

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290 gtt tca gtc ttc gtg tgg ctg ttg gcg ctg ttt ctg gct cta cct gcg      528
291 Val Ser Val Phe Val Trp Leu Leu Ala Leu Phe Leu Ala Leu Pro Ala
292          165          170          175
294 ctc ctt ttc agc cgg gac ggg cca cgt gaa ggc caa cga cgc tgt cgg      576
295 Leu Leu Phe Ser Arg Asp Gly Pro Arg Glu Gly Gln Arg Arg Cys Arg
296          180          185          190
298 ctc att ttt ccc gaa agc ctc acg cag act gtg aaa ggg gca agc gca      624
299 Leu Ile Phe Pro Glu Ser Leu Thr Gln Thr Val Lys Gly Ala Ser Ala
300          195          200          205
302 gtg gcg cag gtg gtc ctc ggc ttc gcg ctc cct ctg ggc gtc atg gca      672
303 Val Ala Gln Val Val Leu Gly Phe Ala Leu Pro Leu Gly Val Met Ala
304          210          215          220
306 gcc tgt tat gcg ctc ctg ggc cgc acg ctt ctg gcc gcc agg ggg cca      720
307 Ala Cys Tyr Ala Leu Leu Gly Arg Thr Leu Leu Ala Ala Arg Gly Pro
308 225          230          235          240
310 gag cgg cgg cgt gca ctg cgc gtc gtg gtg gct ttg gtg gtg gcc ttc      768
311 Glu Arg Arg Arg Ala Leu Arg Val Val Val Ala Leu Val Val Ala Phe
312          245          250          255
314 gtg gtg ctg cag ttg ccc tac agc ctt gcc ctg ctg ctg gat aca gcc      816
315 Val Val Leu Gln Leu Pro Tyr Ser Leu Ala Leu Leu Leu Asp Thr Ala
316          260          265          270
318 gat cta ctg gca gcc cgc gag cgg agc tgc tcc tcc agc aag cgc aag      864
319 Asp Leu Leu Ala Ala Arg Glu Arg Ser Cys Ser Ser Ser Lys Arg Lys
320          275          280          285
322 gat cta gct ttg ctg gtc acc ggc ggc ttg acc ctg gtc cgt tgc agc      912
323 Asp Leu Ala Leu Leu Val Thr Gly Gly Leu Thr Leu Val Arg Cys Ser
324          290          295          300
326 ctc aat ccg gtg ctt tat gcc ttt ttg ggc ctg cgt ttc cgc cgg gac      960
327 Leu Asn Pro Val Leu Tyr Ala Phe Leu Gly Leu Arg Phe Arg Arg Asp
328 305          310          315          320
330 ctg cgg agg ctg ctc cag ggc gga gga tgc agc ccg aag ccc aac cct      1008
331 Leu Arg Arg Leu Leu Gln Gly Gly Gly Cys Ser Pro Lys Pro Asn Pro
332          325          330          335
334 cgt ggc cgc tgc ccc cgt cga ctc cgc ctt tct tcc tgc tct gct cct      1056
335 Arg Gly Arg Cys Pro Arg Arg Leu Arg Leu Ser Ser Cys Ser Ala Pro
336          340          345          350
338 act gag acc cac agt ctc tct tgg gac aac tag      1089
339 Thr Glu Thr His Ser Leu Ser Trp Asp Asn
340          355          360
343 <210> SEQ ID NO: 4
344 <211> LENGTH: 362
345 <212> TYPE: PRT
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354 Tyr Asp Glu Glu Ala Tyr Ser Val Gly Pro Leu Pro Glu Leu Cys Tyr
355          20          25          30
358 Lys Ala Asp Val Gln Ala Phe Ser Arg Ala Phe Gln Pro Ser Val Ser

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**VERIFICATION SUMMARY**

DATE: 04/12/2002

PATENT APPLICATION: US/09/898,751A

TIME: 15:01:07

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L:18 M:270 C: Current Application Number differs, Replaced Current Application Number